

Freeform Search

Database:

US Pre-Grant Publication Full-Text Database
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 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Term:

L9 and (methyl or alkyl or alkyloxy or aryl)

Display: Documents in Display Format: Starting with Number

Generate: ☐ Hit List ☒ Hit Count ☐ Side by Side ☐ Image

Search

Clear

Interrupt

Search History

DATE: Wednesday, April 21, 2004 [Printable Copy](#) [Create Case](#)

Set Name	Query	Hit Count	Set Name
side by side			result set
	DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ		
L10	L9 and (methyl or alkyl or alkyloxy or aryl)	6	L10
L9	(primer\$1 or oligonucleotide\$1) near5 no\$1 complementary near5 modif\$7	10	L9
L8	L7 and 2 end and 3 end	5	L8
L7	L6 and DNA polymerase\$1	38	L7
L6	L5 and (alkyl or alkyloxy or alkylamino or aryl or aryloxy)	44	L6
L5	L4 and modif\$7 nucleotide\$1	134	L5
L4	(primer\$1 or oligonucleotide\$1 or probe\$1) near5 no\$1 complementary	1079	L4
L3	l1 and ((no\$1 or less) near5 exten\$5)	6	L3
L2	L1 and exten\$5	6	L2
L1	(primer\$1 or oligonucleotide\$1 or probe\$1 or nucleic acid sequence\$1) near5 no\$1 complementary near5 modif\$3 near5 nucleotide\$1	6	L1

END OF SEARCH HISTORY

10026952

***** STN Columbus *****

FILE 'HOME' ENTERED AT 12:32:24 ON 21 APR 2004

=> file medline caplus biosis embase

COST IN U.S. DOLLARS

SINCE FILE

ENTRY

TOTAL

SESSION

FULL ESTIMATED COST

0.21

0.21

FILE 'MEDLINE' ENTERED AT 12:32:39 ON 21 APR 2004

FILE 'CAPLUS' ENTERED AT 12:32:39 ON 21 APR 2004

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

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FILE 'BIOSIS' ENTERED AT 12:32:39 ON 21 APR 2004

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FILE 'EMBASE' ENTERED AT 12:32:39 ON 21 APR 2004

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=> s (primer1 or oligonucleotide1)(10a)no# complementary(10a)modif7 nucleotide1
1 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.

For a list of commands available to you in the current file, enter

"HELP COMMANDS" at an arrow prompt (=>).

=> s (primer# or oligonucleotide#)(10a)no# complementary(10a)modif#####
nucleotide#

L1 0 (PRIMER# OR OLIGONUCLEOTIDE#)(10A) NO# COMPLEMENTARY(10A) MODIF#
NUCLEOTIDE#

=> s (primer# or oligonucleotide#)(P)no# complementary(P)modif##### nucleotide#
L2 1 (PRIMER# OR OLIGONUCLEOTIDE#)(P) NO# COMPLEMENTARY(P) MODIF#####
NUCLEOTIDE#

=> d l2 bib ab kwic

L2 ANSWER 1 OF 1 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1976:212966 BIOSIS

DN PREV197662042966; BA62:42966

TI STUDIES OF THE COMPLEX BETWEEN TRANSFER RNA WITH COMPLEMENTARY ANTI CODONS
PART 1 ORIGINS OF ENHANCED AFFINITY BETWEEN COMPLEMENTARY TRIPLETS.

AU GROSJEAN H; SOLL D G; CROTHERS D M

SO Journal of Molecular Biology, (1976) Vol. 103, No. 3, pp. 499-519.

CODEN: JMOBAK. ISSN: 0022-2836.

DT Article

FS BA

LA Unavailable

AB The temperature-jump method was used to study the complex between yeast tRNAPhe and Escherichia coli tRNAGlu, which have the complementary anticodons GmAA and s2UUC, respectively. The binding constant ($3.6 \times 10^5 \text{ M}^{-1}$ at 25°C) is about 6 orders of magnitude larger than expected for 2 complementary trinucleotides. The association rate constant ($3 \times 10^6 \text{ M}^{-1}$ at 25°C) is similar to typical values observed for **oligonucleotides**, so the enhanced affinity in the tRNA · tRNA complex is due entirely to a much slower dissociation than expected for a 3 base-pair helix. An association enthalpy of -25 kcal/mol , nearly twice as large as expected for 2 stacking interactions in a 3 base-pair helix was found. The association entropy ($-58 \text{ cal/deg per mol}$) is close to the expected value. The reaction occurs with a single relaxation and therefore does not involve any slow reorganization of the tRNA molecule. Structural variations were studied to investigate the

origin of affinity enhancement. The following general factors are important. The loop constraint, or closure of the 2 anticodon sequences into hairpin loops, accounts for about a factor 50 in the affinity. Dangling ends, or **non-complementary** nucleotides at the end of the double helix contribute strongly to the affinity. **Modified nucleotides**, like the Y base, in the dangling ends can contribute a special stabilization of up to a factor of 7. These observations can be understood in terms of a model in which the short 3 base-pair helix is sandwiched between stacked bases and hence stabilized. The potential importance of loop-loop interactions and stacking effects for codon-anticodon bonding is emphasized. A possible simple physical basis may exist for the evolutionary choice of a triplet coding system.

AB. . . complementary trinucleotides. The association rate constant ($3 + 106 \text{ M}^{-1}$ at 25° C) is similar to typical values observed for **oligonucleotides**, so the enhanced affinity in the tRNA · tRNA complex is due entirely to a much slower dissociation than expected. . . of the 2 anticodon sequences into hairpin loops, accounts for about a factor 50 in the affinity. Dangling ends, or **non-complementary** nucleotides at the end of the double helix contribute strongly to the affinity. **Modified nucleotides**, like the Y base, in the dangling ends can contribute a special stabilization of up to a factor of 7.. . .

```
=> s (primer# or oligonucleotide#) (P) (no# complementary or no#
hybridiz#####) (p) modif##### nucleotide#
L3      1 (PRIMER# OR OLIGONUCLEOTIDE#) (P) (NO# COMPLEMENTARY OR NO# HYBRID
        IZ#####) (P) MODIF##### NUCLEOTIDE#
```

```
=> d l3 bib ab kwic
```

```
L3  ANSWER 1 OF 1  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN  1976:212966  BIOSIS
DN  PREV197662042966; BA62:42966
TI  STUDIES OF THE COMPLEX BETWEEN TRANSFER RNA WITH COMPLEMENTARY ANTI CODONS
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DT  Article
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AB  The temperature-jump method was used to study the complex between yeast
    tRNAPhe and Escherichia coli tRNAGlu, which have the complementary
    anticodons GmAA and s2UUC, respectively. The binding constant ( $3.6 + 105 \text{ M}^{-1}$  at  $25^\circ \text{ C}$ ) is about 6 orders of magnitude larger
    than expected for 2 complementary trinucleotides. The association rate
    constant ( $3 + 106 \text{ M}^{-1}$  at  $25^\circ \text{ C}$ ) is similar to typical values
    observed for oligonucleotides, so the enhanced affinity in the
    tRNA · tRNA complex is due entirely to a much slower dissociation
    than expected for a 3 base-pair helix. An association enthalpy of -25
    kcal/mol, nearly twice as large as expected for 2 stacking interactions in
    a 3 base-pair helix was found. The association entropy (-58 cal/deg per
    mol) is close to the expected value. The reaction occurs with a single
    relaxation and therefore does not involve any slow reorganization of the
    tRNA molecule. Structural variations were studied to investigate the
    origin of affinity enhancement. The following general factors are
    important. The loop constraint, or closure of the 2 anticodon sequences
    into hairpin loops, accounts for about a factor 50 in the affinity.
    Dangling ends, or non-complementary nucleotides at the
    end of the double helix contribute strongly to the affinity.
Modified nucleotides, like the Y base, in the dangling
    ends can contribute a special stabilization of up to a factor of 7. These
    observations can be understood in terms of a model in which the short 3
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```
=> s (primer# or oligonucleotide#)(p)modif##### nucleotide#
L4      444 (PRIMER# OR OLIGONUCLEOTIDE#)(P) MODIF##### NUCLEOTIDE#
```

```
=> s l4 and (no# complementary or no# hybridiz#####)
L5      5 L4 AND (NO# COMPLEMENTARY OR NO# HYBRIDIZ#####)
```

```
=> dup rem l5
PROCESSING COMPLETED FOR L5
L6      2 DUP REM L5 (3 DUPLICATES REMOVED)
```

```
=> d l6 1-2 bib ab kwic
```

```
L6      ANSWER 1 OF 2      MEDLINE on STN      DUPLICATE 1
AN      96428850      MEDLINE
DN      PubMed ID: 8831952
TI      Recognition of the primers containing different modified
nucleotide units by the Klenow fragment of DNA polymerase I from E
coli.
AU      Kolocheva T I; Levina A S; Nevinsky G A
CS      Novosibirsk Institute of Bioorganic Chemistry, Siberian Division of the
Russian Academy of Sciences, Russia.
SO      Biochimie, (1996) 78 (3) 201-3.
Journal code: 1264604. ISSN: 0300-9084.
CY      France
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Priority Journals
EM      199612
ED      Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961203
AB      A comparison of Km values and maximal rates of extension (Vmax) for
primers containing different modified bases or mismatches, and fully
complementary primers of the same length catalyzed by the Klenow fragment
of E coli DNA polymerase I was carried out. Base modifications include
T-T dimers and apurinic sites. In the case of mismatch, the number of
complementary bases from the 3'-terminus to the non-
complementary nucleotide determines the efficiency of substrate
incorporation, which is a measure of degree of interaction of the enzyme
with its primer template. Differently, removal of one base in any
position from the 3'-terminus of the primer is equivalent to shortening of
the primer by one nucleotide unit, and decreases the affinity to the
enzyme by 1.8-fold. Since apurinic sites fail to interfere with the
efficiency of DNA synthesis, we suppose that the Klenow fragment of E coli
DNA polymerase I does not participate in the correction of DNAs containing
apurinic nucleotides units. Finally, the efficiency of elongation of the
d(p primer was shown to decrease with an increase in T-T dimers in the
primer. When the d(pT)10m primer contains about 2.6 T-T dimers per
```

TI molecule, the efficiency of its elongation decreases by a factor of 8-18.
Recognition of the **primers** containing different **modified nucleotide** units by the Klenow fragment of DNA polymerase I from E coli.

AB . . . T-T dimers and apurinic sites. In the case of mismatch, the number of complementary bases from the 3'-terminus to the **non-complementary** nucleotide determines the efficiency of substrate incorporation, which is a measure of degree of interaction of the enzyme with its. . .

L6 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

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